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EPAB,DWPI	l12 and tufano	0	L15
EPAB,DWPI	l12 and porin	0	L14
EPAB,DWPI	l12 and doig	0	L13
EPAB,DWPI	9640893	3	L12
EPAB,DWPI	40893	11	L11
EPAB,DWPI	l8 and doig	3	L10
EPAB,DWPI	l8 and porin	0	L9
EPAB,DWPI	l7 and astra	7	L8
EPAB,DWPI	l3 and smith.in.	21	L7
EPAB,DWPI	l1 and pylori.in.	0	L6
EPAB,DWPI	l1 and smith.in.	0	L5
EPAB,DWPI	l1 and astra	0	L4
EPAB,DWPI	helicobacter$.ti.	657	L3
EPAB,DWPI	helicobacter?.ti.	0	L2
EPAB,DWPI	helicobacter? and astra	0	L1

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Set	Items	Description
S1	13	AU=DOIG ? AND PORIN?
S2	5	RD (unique items)

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2/9/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08540347 95197292
Isolation and characterization of a family of porin **proteins from Helicobacter pylori.**
Exner MM; **Doig P** ; Trust TJ; Hancock RE
Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.
Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72, ISSN 0019-9567 Journal Code: GO7
Contract/Grant No.: R01AI29927-01A2, AI, NIAID
Languages: ENGLISH
Document type: JOURNAL ARTICLE
JOURNAL ANNOUNCEMENT: 9506
Subfile: INDEX MEDICUS
Two-dimensional gel electrophoresis was used to identify heat-modifiable outer membrane proteins, which were candidates for **porins** , from Helicobacter pylori membrane preparations. Four such proteins with apparent molecular masses of 48, 49, 50, and 67 kDa were isolated. The four proteins copurified together after selective detergent solubilizations followed by anion-exchange chromatography, and each protein was ultimately purified to homogeneity by gel purification. These proteins were then tested for pore-forming ability with a planar lipid bilayer model membrane system. All four proteins appeared to be present as monomers, and they formed pores with low single-channel conductances in 1.0 M KCl of 0.36, 0.36, 0.30, and 0.25 nS, respectively, for the 48-, 49-, 50-, and 67-kDa proteins which we propose to designate HopA, HopB, HopC, and HopD. N-terminal amino acid sequence analyses showed a high degree of homology among all four proteins, and it appears that these proteins constitute a family of related **porins** in H. pylori.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: Helicobacter pylori--Chemistry--CH; ***Porins** --Isolation and Purification--IP; Amino Acid Sequence; Electric Conductivity; Electrophoresis, Gel, Two-Dimensional; Heat; Helicobacter pylori --Physiology--PH; Ion Channels--Chemistry--CH; Ion Channels--Isolation and Purification--IP; Molecular Sequence Data; Molecular Weight; Multigene Family; **Porins** --Chemistry--CH; Sequence Alignment; Sequence Homology, Amino Acid
CAS Registry No.: 0 (Ion Channels); 0 (Porins)
Gene Symbol: hopB; hopC; hopD; hopA

2/9/4 (Item 4 from file: 155)

08021587 95012645

Identification of surface-exposed outer membrane antigens of Helicobacter pylori.

Doig P ; Trust TJ
Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Infection and immunity (UNITED STATES) Oct 1994, 62 (10) p4526-33, ISSN 0019-9567 Journal Code: GO7
Contract/Grant No.: 1RO1AI29927-01A2, AI, NIAID
Languages: ENGLISH
Document type: JOURNAL ARTICLE
JOURNAL ANNOUNCEMENT: 9501
Subfile: INDEX MEDICUS

Despite the potential significance of surface-localized antigens in the colonization by and disease processes of Helicobacter pylori, few such components have been unequivocally identified and/or characterized. To further investigate the surface of this bacterium, monoclonal antibodies (MAbs) to a sarcosine-insoluble outer membrane fraction prepared from H. pylori NCTC 11637 were raised. MAbs were selected on the basis of their surface reactivity to whole cells by enzyme-linked immunosorbent assay, immunofluorescence, and immunoelectron microscopy. By use of this selection protocol, 14 surface-reactive MAbs were chosen. These MAbs were used to identify six protein antigens (molecular masses, 80, 60, 51, 50, 48, and 31 kDa), all of which were localized within or associated with the outer membrane. Two of the MAbs recognized the core region of lipopolysaccharide (LPS). Only these two anti-LPS MAbs also recognized the flagellar sheath, indicating a structural difference between the sheath and outer membrane. Three of the protein antigens (80, 60, and 51 kDa) were strain specific, while the other three antigens were present in other strains of H. pylori. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins** . A conserved 31-kDa protein may represent another species of **porin** . A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H. pylori outer membranes with minimal inner membrane contamination is described. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis showed that the protein content of the H. pylori outer membrane is similar structurally to those of other species of Helicobacter but markedly different from those of taxonomically related Campylobacter spp. and Escherichia coli. H. pylori also appeared to lack peptidoglycan-associated proteins.

Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Antigens, Bacterial--Analysis--AN; *Bacterial Outer Membrane Proteins--Analysis--AN; *Helicobacter pylori--Immunology--IM; Antibodies, Monoclonal--Immunology--IM; Antigens, Surface--Analysis--AN; Mice; Mice, Inbred BALB C; Molecular Weight
CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Antigens, Bacterial) ; 0 (Antigens, Surface); 0 (Bacterial Outer Membrane Proteins)
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Articles:

Identification of surface-exposed outer membrane antigens of Helicobacter pylori.

Doig P ; Trust TJ
Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Infection and immunity (UNITED STATES) Oct 1994, 62 (10) p4526-33, ISSN 0019-9567 Journal Code: GO7
Contract/Grant No.: 1RO1AI29927-01A2, AI, NIAID
Languages: ENGLISH
Document type: JOURNAL ARTICLE
JOURNAL ANNOUNCEMENT: 9501
Subfile: INDEX MEDICUS

Despite the potential significance of surface-localized antigens in the colonization by and disease processes of Helicobacter pylori, few such components have been unequivocally identified and/or characterized. To further investigate the surface of this bacterium, monoclonal antibodies (MAbs) to a sarcosine-insoluble outer membrane fraction prepared from H. pylori NCTC 11637 were raised. MAbs were selected on the basis of their surface reactivity to whole cells by enzyme-linked immunosorbent assay, immunofluorescence, and immunoelectron microscopy. By use of this selection protocol, 14 surface-reactive MAbs were chosen. These MAbs were used to identify six protein antigens (molecular masses, 80, 60, 51, 50, 48, and 31 kDa), all of which were localized within or associated with the outer membrane. Two of the MAbs recognized the core region of lipopolysaccharide (LPS). Only these two anti-LPS MAbs also recognized the flagellar sheath, indicating a structural difference between the sheath and outer membrane. Three of the protein antigens (80, 60, and 51 kDa) were strain specific, while the other three antigens were present in other strains of H. pylori. Both the 51- and 48-kDa antigens were heat modifiable and likely are **porins** . A conserved 31-kDa protein may represent another species of **porin** . A method involving sucrose density ultracentrifugation and Triton extraction that allows the preparation of H. pylori outer membranes with minimal inner membrane contamination is described. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis showed that the protein content of the H. pylori outer membrane is similar structurally to those of other species of Helicobacter but markedly different from those of taxonomically related Campylobacter spp. and Escherichia coli. H. pylori also appeared to lack peptidoglycan-associated proteins.

Isolation and characterization of a family of porin **proteins from Helicobacter pylori.**

Exner MM; **Doig P** ; Trust TJ; Hancock RE

Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.

Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72, ISSN 0019-9567 Journal Code: GO7

Contract/Grant No.: R01AI29927-01A2, AI, NIAID

Languages: ENGLISH

Document type: JOURNAL ARTICLE

JOURNAL ANNOUNCEMENT: 9506

Subfile: INDEX MEDICUS

Two-dimensional gel electrophoresis was used to identify heat-modifiable outer membrane proteins, which were candidates for **porins** , from Helicobacter pylori membrane preparations. Four such proteins with apparent molecular masses of 48, 49, 50, and 67 kDa were isolated. The four proteins copurified together after selective detergent solubilizations followed by anion-exchange chromatography, and each protein was ultimately purified to homogeneity by gel purification. These proteins were then tested for pore-forming ability with a planar lipid bilayer model membrane system. All four proteins appeared to be present as monomers, and they formed pores with low single-channel conductances in 1.0 M KCl of 0.36, 0.36, 0.30, and 0.25 nS, respectively, for the 48-, 49-, 50-, and 67-kDa proteins which we propose to designate HopA, HopB, HopC, and HopD. N-terminal amino acid sequence analyses showed a high degree of homology among all four proteins, and it appears that these proteins constitute a family of related **porins** in H. pylori.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S

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*File 155: This file will be reloaded. Accession numbers will change.

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Set	Items	Description
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S2	27	S1/1996:2002
S3	16	S1 NOT S2

?t s3/9/5 6

3/9/5
DIALOG(R)File 155:MEDLINE(R)

Isolation and characterization of a family of porin proteins from Helicobacter pylori .

Exner MM; Doig P; Trust TJ; Hancock RE

Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.

Infection and immunity (UNITED STATES) Apr 1995, 63 (4) p1567-72, ISSN 0019-9567 Journal Code: GO7

Contract/Grant No.: R01AI29927-01A2, AI, NIAID

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Two-dimensional gel electrophoresis was used to identify heat-modifiable outer membrane proteins, which were candidates for porins, from Helicobacter pylori membrane preparations. Four such proteins with apparent molecular masses of 48, 49, 50, and 67 kDa were isolated. The four proteins copurified together after selective detergent solubilizations followed by anion-exchange chromatography, and each protein was ultimately purified to homogeneity by gel purification. These proteins were then tested for pore-forming ability with a planar lipid bilayer model membrane system. All four proteins appeared to be present as monomers, and they formed pores with low single-channel conductances in 1.0 M KCl of 0.36, 0.36, 0.30, and 0.25 nS, respectively, for the 48-, 49-, 50-, and 67-kDa proteins which we propose to designate HopA, HopB, HopC, and HopD. N-terminal amino acid sequence analyses showed a high degree of homology among all four proteins, and it appears that these proteins constitute a family of related porins in H. pylori.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Helicobacter pylori--chemistry--CH; *Porins--isolation and purification--IP; Amino Acid Sequence; Electric Conductivity; Electrophoresis, Gel, Two-Dimensional; Heat; Helicobacter pylori --physiology--PH; Ion Channels--chemistry--CH; Ion Channels--isolation and purification--IP; Molecular Sequence Data; Molecular Weight; Multigene Family; Porins--chemistry--CH; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Ion Channels); 0 (Porins)

Gene Symbol: ist/GeneSymbol hopA; ist/GeneSymbol hopB; ist/GeneSymbol hopC; ist/GeneSymbol hopD

Record Date Created: 19950420

?b

Progress in defining the inflammatory cascade.

Figura N
School of Gastroenterology, University of Siena, Policlinico Le Scotte, Italy.

European journal of gastroenterology & hepatology (ENGLAND) Apr 1995, 7 (4) p296-302, ISSN 0954-691X Journal Code: B9X
Languages: ENGLISH
Document type: Journal Article; Review; Review, Tutorial
Record type: Completed
Subfile: INDEX MEDICUS

Helicobacter pylori infection is characterized by an inflammatory response in the gastric epithelium, the intensity of which appears to be type-strain specific. Infections caused by Type 1 H. pylori organisms, i.e., those expressing VacA (the cytotoxin) and CagA (the cytotoxin-associated protein), are associated with a strong polymorph mucosal infiltration in vivo, and with increased secretion of interleukin-8 by epithelial cells. The inflammatory potential of Type II strains (non-cytotoxic, VacA- and CagA-negative) is probably less pronounced. The small urease subunit, **porins** , and other substances produced by H. **pylori** show neutrophil chemotactic activities in vitro. These bacterial components promote the adhesion of polymorphs to endothelial cells and stimulate polymorphs to generate oxygen reactive metabolites. This can severely damage the gastroduodenal mucosa. (38 Refs.)

Tags: Human
Descriptors: *Helicobacter Infections--metabolism--ME; *Helicobacter pylori; Helicobacter pylori--metabolism--ME; Inflammation--metabolism--ME; Interleukin-8--metabolism--ME
CAS Registry No.: 0 (Interleukin-8)
Record Date Created: 19950807

Cell surface characteristics of Helicobacter pylori.

Moran AP
Department of Microbiology, University College, Galway, Ireland.

FEMS immunology and medical microbiology (NETHERLANDS) Feb 1995, 10 (3-4) p271-80, ISSN 0928-8244 Journal Code: BP1
Languages: ENGLISH
Document type: Journal Article; Review; Review, Academic
Record type: Completed
Subfile: INDEX MEDICUS

Helicobacter pylori is an important gastroduodenal pathogen of humans. Immunological and structural studies have been performed on the phospholipids, lipopolysaccharides (LPS) and some surface proteins of H. pylori strains. H. pylori LPS has, in general, low immunological activity and this property may aid the survival of this chronic infection. Nevertheless, H. pylori LPS has been found to influence the quality of gastric mucin and to stimulate pepsinogen secretion, thereby contributing to gastric disease. A number of putative adhesins of the bacterium have been described. This multiplicity of adhesins may reflect that H. pylori adherence is a multi-step process involving different interactions, and that different adhesins may mediate adherence to various sites in gastric tissue. (54 Refs.)

Tags: Animal; Human; Support, Non-U.S. Gov't
Descriptors: *Bacterial Outer Membrane Proteins--chemistry--CH; *Helicobacter pylori--physiology--PH; *Lipopolysaccharides--chemistry--CH; *Lipopolysaccharides--immunology--IM; Adhesins, Bacterial--chemistry--CH; Adhesins, Bacterial--physiology--PH; Bacterial Capsules--physiology--PH; Bacterial Outer Membrane Proteins--physiology--PH; Carbohydrate Sequence; Cell Wall--chemistry--CH; Cell Wall--physiology--PH; Heat-Shock Proteins --chemistry--CH; **Helicobacter pylori** --pathogenicity--PY; Molecular Sequence Data; **Porins** --chemistry--CH; **Porins** --immunology--IM; Rats
CAS Registry No.: 0 (Adhesins, Bacterial); 0 (Bacterial Capsules); 0 (Bacterial Outer Membrane Proteins); 0 (Heat-Shock Proteins); 0 (Lipopolysaccharides); 0 (Porins)
Record Date Created: 19950713